

Supplementary Table 1. Demographic characteristics of exploration panel and validation panel.

	Exploration panel			Validation panel		
	PBC(n=60)	HC(n=80)	P	PBC(n=19)	HC(n=34)	P
Age,median years(min-max)	51.5(22-78)	48(25-65)	0.49	52(32-70)	46.5(34-63)	0.04
Gender,Female(%)	55(91.7%)	67(83.8%)	0.17	12(63.2%)	24(70.6%)	0.58
BMI,median kg/m2(min-max)	22.63(17.58-29.04)	22.43(16.73-29.37)	0.63	21.76(17.8-27.89)	22.48(16.23-29.07)	0.59
ALT,U/L,median(min-max)	61(8-276)			85(22.6-760.8)		
AST,U/L,median(min-max)	49(9.1-216)			72(24.3-510)		
AKP,U/L,median(min-max)	196(46.9-1416)			274(68.1-870)		
GGT,U/L,median(min-max)	190(13-1560)			187(22.6-726)		
TB,umol/L,median(min-max)	14.45(5.1-250.3)			15.5(8.9-51.3)		
IgM,g/L,medain(min-max)	2.875(0.79-9.6)			3.04(1.33-6.08)		
IgG,g/L,medain(min-max)	15.35(10.3-30.1)			15.85(12.6-28.2)		
AMA,+/-,n(+%)	56/4,93.3%			16/3,84.2%		
gp210,+/-,n(+%)	26/34,43.3%			8/11,42.1%		
sp100,+/-,n(+%)	2/58,3.3%			6/13,31.6%		

Wilcoxon rank-sum test was used to compare age and BMI between naïve PBC and healthy controls; fisher's exact test was used to compare gender distribution between PBC and controls.

Supplementary Table 2. Association analysis between microbiome and PBC at genus level.

Family	Genus	Mean relative abundance		Wilcoxon rank-sum test		Logistic regression		Fold change
		PBC (n=60)	Control (n=80)	P	Pfdr	P	Pfdr	
Enterobacteriaceae	unknown	0.071	0.011	7.50E-07	4.65E-05	2.23E-05	1.90E-04	6.4
Pseudomonadaceae	Pseudomonas	2.56E-04	4.06E-05	1.18E-06	4.65E-05	1.40E-05	1.90E-04	6.3
Veillonellaceae	Veillonella	0.019	1.97E-03	1.06E-04	0.003	0.002	0.008	9.6
Clostridiaceae	Clostridium	7.80E-04	7.29E-05	9.52E-04	0.011	0.002	0.008	10.7
Ruminococcaceae	Oscillospira	0.007	0.011	6.58E-04	0.010	0.003	0.010	0.6
Alcaligenaceae	Sutterella	0.018	0.027	6.38E-04	0.010	0.004	0.010	0.7
Lactobacillaceae	Lactobacillus	7.93E-04	3.96E-05	0.002	0.017	0.012	0.024	20.0
Pasteurellaceae	Haemophilus	0.010	0.002	0.002	0.017	0.013	0.024	6.6
Streptococcaceae	Streptococcus	5.19E-03	1.29E-03	0.003	0.022	0.010	0.024	4.0
Enterobacteriaceae	Klebsiella	3.52E-04	6.56E-05	7.74E-04	0.010	0.019	0.032	5.4
Bacteroidaceae	Bacteroides	0.433	0.530	0.006	0.036	0.034	0.053	0.8
Ruminococcaceae	Faecalibacterium	0.011	0.015	0.002	0.017	0.038	0.054	0.7

Logistic regression test was adjusted for covariates including age, gender and BMI.

Supplementary Table 3. Six PBC-associated genera were reversed after UDCA treatment.

Family	Genus	Mean relative abundance			P value
		PBC (N=37)		Control (n=114)	
		Before UDCA	After UDCA		
Pseudomonadaceae	Pseudomonas	2.73E-04	1.12E-04	2.96E-05	0.003
Streptococcaceae	Streptococcus	0.005	0.003	0.001	0.006
Pasteurellaceae	Haemophilus	0.011	0.003	0.002	0.010
Ruminococcaceae	Oscillospira	0.006	0.012	0.010	2.51E-04
Alcaligenaceae	Sutterella	0.016	0.035	0.025	1.01E-04
Bacteroidaceae	Bacteroides	0.369	0.450	0.501	0.046

Paired wilcoxon test was used to compare the relative abundances of genera before and after UDCA treatment in PBC.

Supplementary Table 4. Blast results for the OTU sequences of the two genera in family of Enterobacteriaceae.

Query OTU#	Blast hit		Alignment		
	Description	Accession	Max Score	E-value	Identity
OTU1	Klebsiella quasipneumoniae subsp. quasipneumoniae strain 01A030	NR_134062.1	815	0	99%
OTU1	Klebsiella pneumoniae strain DSM 30104	NR_117683.1	815	0	99%
OTU1	Klebsiella pneumoniae subsp. rhinoscleromatis strain ATCC 13884	NR_114507.1	815	0	99%
OTU1	Klebsiella pneumoniae subsp. rhinoscleromatis strain R-70	NR_037084.1	815	0	99%
OTU2	Escherichia coli strain JCM 1649	NR_112558.1	821	0	99%
OTU2	Escherichia coli strain NBRC 102203	NR_114042.1	817	0	99%
OTU2	Escherichia coli strain U 5/41	NR_024570.1	817	0	99%
OTU2	Escherichia fergusonii strain ATCC 35469	NR_074902.1	821	0	99%
OTU2	Escherichia fergusonii strain ATCC 35469	NR_027549.1	821	0	99%
OTU2	Escherichia fergusonii strain NBRC 102419	NR_114079.1	821	0	99%
OTU2	Escherichia vulneris strain ATCC 33821	NR_119109.1	821	0	99%
OTU2	Shigella flexneri strain ATCC 29903	NR_026331.1	821	0	99%
OTU2	Shigella sonnei strain CECT 4887	NR_104826.1	821	0	99%
OTU3	Enterobacter hormaechei strain 0992-77	NR_042154.1	811	0	99%
OTU3	Enterobacter cloacae subsp. dissolvens strain LMG 2683	NR_044978.1	811	0	99%
OTU4	Klebsiella variicola strain F2R9	NR_025635.1	794	0	99%
OTU4	Klebsiella pneumoniae strain DSM 30104	NR_117686.1	789	0	99%
OTU4	Klebsiella pneumoniae strain JCM1662	NR_112009.1	789	0	99%

*database: 16s rRNA